Claims

1. DNA sequences which code for a polypeptide with the amino acid sequence shown in SEQ ID no. 2 or for an analogue or derivative of the polypeptide according to SEQ ID no. 2, in which one or more amino acids have been deleted, added or replaced by other amino acids, wherein the enzymatic action of the polypeptide is retained, and which sequences originate from parasites, wherein sequence variations occurring within the framework of natural strain variability are included.

2. DNA sequences which code for a polypeptide with the amino acid sequence shown in SEQ ID no. 4 or for an analogue or derivative of the polypeptide according to SEQ ID no. 4, in which one or more amino acids have been deleted, added or replaced by other amino acids, wherein the enzymatic action of the polypeptide is retained, and which sequences originate from parasites, wherein sequence variations occurring within the framework of natural strain variability are included.

3. DNA sequences which code for a polypeptide with the amino acid sequence shown in SEQ ID no. 6 or for an analogue or derivative of the polypeptide according to SEQ ID no. 6, in which one or more amino acids have been deleted, added or replaced by other amino acids wherein the catalytic function of the polypeptide is retained.

4. DNA sequence according to one of claims 1 to 3, characterised in that it also comprises functional regulation signals, in particular promoters, operators, enhancers, ribosomal binding sites.

5. DNA sequence with the following sub-sequences

i) promoter which is active in viruses, eukaryotes and prokaryotes and ensures the formation of an RNA in the intended target tissue or target cells,

ii) DNA sequences according to one of claims 1 to 3,

iii) 3' untranslated sequence which, in viruses, eukaryotes and prokaryotes, results in the addition of poly(A) residues onto the 3' end of the RNA.

Sub a1

6. Process for the production of transgenic viruses, eukaryotes and prokaryotes for modifying the isoprenoid content, characterised in that a DNA sequence according to claim 4 or 5 is transferred and incorporated into the genome of viruses, eukaryotic and prokaryotic cells with or without use of a vector.

7. Transgenic systems, in particular plants and plant cells which contain one or more DNA sequences according to claims 1 to 5 as "foreign" or "additional" DNA, which sequences are expressed.

8. Expression vector containing one or more DNA sequences according to claims 1 to 5.

9. Protein which is involved in the 1-deoxy-D-xylulose 5-phosphate metabolic pathway and a) is coded by DNA sequences SEQ ID no. 1, 3 or 5 or b) is coded by DNA sequences which hybridise with DNA sequences SEQ ID no. 1, 3, 5 or fragments of these DNA sequences in the DNA region which codes for the mature protein.

10. Protein according to claim 9, obtainable from the culture supernatants of parasites or from the disrupted parasites and purification by chromatographic and electrophoretic methods.

Sub a2

11. Protein according to one of claims 9 and 10, characterised in that it a) is the product of viral, prokaryotic or eukaryotic expression of exogenous DNA, b) is coded by sequences SEQ ID no. 1, 3 or 5 or is coded by DNA sequences which hybridise with DNA sequences SEQ ID no. 1, 3, 5 or fragments of these DNA sequences in the DNA region which codes for the mature protein, or c) is coded by DNA sequences which would hybridise without degeneration of the genetic code with the sequences defined in b) and which code for a polypeptide with a corresponding amino acid sequence.

12. Protein according to one of the preceding claims, characterised in that it comprises the amino acid sequences SEQ ID no. 2, 4 or 6.

13. Process for determining the enzymatic activity of the gcpE protein, characterised in that phosphorylation of a sugar or of a phosphorus sugar or of a precursor of isoprenoid biosynthesis, in

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particular the phosphorylation of 2-C-methyl-D-erythritol, 2-C-methyl-D-erytritol phosphate, in particular 2-C-methyl-D-erythritol 4-phosphate, 2-C-methyl-D-erythrose, 2-C-methyl-D-erythrose phosphate, in particular 2-C-methyl-D-erythrose 4-phosphate, and of phosphate and alcohol precursors, is detected.

14. Process according to claim 13, characterised in that phosphorylation of the following phosphates or alcohols is detected:

$CH_2(OH)-C(CH_3)=C(OH)-CH_2-O-PO(OH)_2$,

$CH_2(OH)-C(CH_3)=C(OH)-CH_2-OH$,

$CH_2(OH)-CH(CH_3)-CO-CH_2-O-PO(OH)_2$,

$CH_2(OH)-CH(CH_3)-CO-CH_2OH$

$CH_2=C(CH_3)-CO-CH_2-O-PO(OH)_2$,

$CH_2=C(CH_3)-CO-CH_2-OH$,

$CH_2=C(CH_3)-CH(OH)-CH_2-O-PO(OH)_2$,

$CH_2=C(CH_3)-CH(OH)-CH_2-OH$,

$CH_2(OH)-C(=CH_2)-C(OH)-CH_2-O-PO(OH)_2$,

$CH_2(OH)-C(=CH_2)-C(OH)-CH_2-OH$

$CHO-CH(CH_3)-CH(OH)-CH_2-O-PO-(OH)_2$,

$CHO-CH(CH_3)-CH(OH)-CH_2-OH$,

$CH_2(OH)-C(OH)(CH_3)-CH=CH-O-PO(OH)_2$,

$CH_2(OH)-C(OH)(CH_3)-CH=CH-OH$

$CH(OH)=C(CH_3)-CH(OH)-CH_2-O-PO(OH)_2$,

$CH(OH)=C(CH_3)-CH(OH)-CH_2-OH$,

$(CH_3)_2HC-CO-CH_2-O-PO(OH)_2$,

$(CH_3)_2HC-CO-CH_2-O-H$,

$(CH_3)_2HC-CH(OH)-CH_2-O-PO(OH)_2$,

$(CH_3)_2HC-CH(OH)-CH_2-O-H$.

15. Process for the combined determination of the enzymatic activity of DOXP synthase and of DOXP reductase, characterised in that the conversion of glyceraldehyde 3-phosphate into 2-C-methylerythritol 4-phosphate is detected.

16. Process for screening a compound for the treatment of infectious processes in humans and animals, wherein the process comprises:

a) provision of a host cell which contains a recombinant expression vector, wherein the vector comprises at least a portion of the oligonucleotide sequence according to SEQ ID no. 1, SEQ ID no. 3 or SEQ ID no. 5 or variants or analogues thereof, and moreover of a compound suspected to have antimycotic, antibiotic, antiparasitic or antiviral action in humans and animals,

b) bringing the host cell into contact with the compound and

c) determining the antimicrobial, antimycotic, antibiotic, antiparasitic or antiviral action of the compound.

17. Process for screening for compounds for treating plants, wherein the process comprises:

a) provision of a host cell which contains a recombinant expression vector, wherein the vector comprises at least a portion of the oligonucleotide sequence according to SEQ ID no. 1, SEQ ID no. 3 or SEQ ID no. 5 or variants or analogues thereof, and moreover of a compound suspected to have antimicrobial,

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antiviral, antiparasitic, bactericidal, fungicidal or herbicidal action in plants,

b) bringing the host cell into contact with the compound and

c) determining the antimicrobial, antiviral, antiparasitic, bactericidal, fungicidal or herbicidal action of the compound.

sub a3

18. Use of DNA according to one of claims 1 to ~~5 or of~~ proteins according to one of ~~claims~~ 9 to 12 or of transgenic ~~systems~~ according to claim 7 for the ~~prevention~~ or treatment of diseases in humans and animals.

add a4